



SEQUENCE LISTING

<110> Gilbert, Michel
Wakarchuk, Warren W.
National Research Council of Canada

<120> Campylobacter Glycosyltransferases for Biosynthesis of Gangliosides and Ganglioside Mimics

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<141> 2001-03-21

<150> US 60/118,213
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<170> PatentIn Ver. 2.1

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biosynthesis locus)

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255																																																																																																																			
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816																																																																																																																		
Asn Ile Asn Phe Lys Lys Ile Lys Glu Asn Ile Tyr Tyr Lys																																																																																																																			
260	265	270		ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864	Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe		275	280	285		aaa gga aaa taa	876	Lys Gly Lys		290		 		<210> 3		<211> 291		<212> PRT		<213> Campylobacter jejuni		 		<220>		<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase		Campylobacter sialyltransferase II (cstII) from C. jejuni		strain OH4384 (ORF 7a of lipooligosaccharide (LOS)		biosynthesis locus)		 		<400> 3		Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile		1 5 10 15		Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln		20 25 30		Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val		35 40 45		Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His		50 55 60		Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn		65 70 75 80		Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr		85 90 95		Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu		100 105 110		Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln		115 120 125		Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly		130 135 140		Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser		145 150 155 160		Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro		165 170 175		Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr		180 185 190		Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu		195 200 205		Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala		210 215 220		Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr		225 230 235 240		Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys		245 250 255									
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ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864																																																																																																																		
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe																																																																																																																			
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285																																																																																																																			
aaa gga aaa taa	876																																																																																																																		
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1 5 10 15																																																																																																																			
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Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val																																																																																																																			
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Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His																																																																																																																			
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Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr																																																																																																																			
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Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr																																																																																																																			
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Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys																																																																																																																			
245 250 255																																																																																																																			

Asn	Ile	Asn	Phe	Lys	Lys	Ile	Lys	Ile	Lys	Glu	Asn	Ile	Tyr	Tyr	Lys
			260			265				270					
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe
			275			280				285					
Lys	Gly	Lys													
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Campylobacter sialyltransferase II (cstII) from C. jejuni
 serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
 biosynthesis locus)

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1			5					10						15		

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Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	
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Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Phe	Lys	Ala	Val	
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Phe	Tyr	Asn	Pro	Gly	Ile	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	
				50				55			60					

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				65				70			75		80			

tac	aac	caa	gct	cat	cta	gaa	aat	ttt	gta	aaa	act	ttt	tac		288	
Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr	
				85				90			95					

gat	tat	ttt	cct	gat	gct	cat	ttg	gga	tat	gat	ttt	ttt	aaa	caa	ctt	336
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu	
				100				105			110					

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Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Leu	Asn	Gln	
				115				120			125					

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Arg	Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Val	Ala	Ile	Ala	Leu	Gly	
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gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu 195 200 205	624
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ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe 275 280 285	864
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Campylobacter sialyltransferase II (cstII) from C. jejuni
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
biosynthesis locus)

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35 40 45
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
50 55 60

Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn
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Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr
					85					90					95
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu
					100					105					110
Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Leu	Asn	Gln
					115					120					125
Arg	Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Val	Ala	Ile	Ala	Leu	Gly
					130					135					140
Tyr	Lys	Glu	Ile	Tyr	Leu	Ser	Gly	Ile	Asp	Phe	Tyr	Gln	Asn	Gly	Ser
					145					150					160
Ser	Tyr	Ala	Phe	Asp	Thr	Lys	Gln	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Pro
					165					170					175
Asp	Phe	Lys	Asn	Asp	Arg	Ser	His	Tyr	Ile	Gly	His	Ser	Lys	Asn	Thr
					180					185					190
Asp	Ile	Lys	Ala	Leu	Glu	Phe	Leu	Glu	Lys	Thr	Tyr	Lys	Ile	Lys	Leu
					195					200					205
Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala
					210					215					220
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr
					225					230					240
Lys	Asp	Ile	Leu	Ile	Pro	Ser	Ser	Glu	Ala	Tyr	Gly	Lys	Phe	Ser	Lys
					245					250					255
Asn	Ile	Asn	Phe	Lys	Ile	Lys	Ile	Lys	Glu	Asn	Ile	Tyr	Tyr	Lys	
					260					265					270
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe
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Lys	Gly	Lys													
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(cstII) from *C. jejuni* serotype O:41

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Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln
20										25					30
ttt	tat	ttt	gaa	gat	aaa	tac	tat	ctt	ggt	aaa	aaa	tgc	aaa	gca	gta
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Ala	Val
35										40					45
ttt	tac	aat	cct	agt	ctt	ttt	gaa	caa	tac	tac	act	tta	aaa	cat	
Phe	Tyr	Asn	Pro	Ser	Leu	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His
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Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr			
85	90	95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt		336	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu			
100	105	110	
aaa gaa ttc aat gct tat ttt aaa cac gaa att tat ttc aat caa		384	
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln			
115	120	125	
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Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly			
130	135	140	
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Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser			
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Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro			
165	170	175	
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180	185	190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac gaa ata aag cta		624	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu			
195	200	205	
tat tgt tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg		672	
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala			
210	215	220	
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Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys			
245	250	255	
aat att aat ttt aaa aat aat aat att aat gaa aat att tat tac aag		816	
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys			
260	265	270	
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275	280	285	
aaa gga aaa taa		876	
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      (cstII) from C. jejuni serotype O:41

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    20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
    35          40          45
Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
    50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
    65          70          75          80
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr
    85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
    100         105         110
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
    115         120         125
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly
    130         135         140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
    145         150         155         160
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
    165         170         175
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
    180         185         190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu
    195         200         205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
    210         215         220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
    225         230         235         240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys
    245         250         255
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
    260         265         270
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
    275         280         285
Lys Gly Lys
    290

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<210> 8
<211> 876
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(876)
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
      (CstII) from C. jejuni O:19

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<400> 8
 atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15

 gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa 96
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30

 ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg 144
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35 40 45

 ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat 192
 Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Leu Lys His
 50 55 60

 tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80

 tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95

 gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110

 aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa 384
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125

 aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga 432
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140

 tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca 480
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160

 tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct 528
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175

 gat ttt aaa aat gat cgc tcg cac tat atc gga cat agt aaa aat aca 576
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190

 gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta 624
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205

 tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg 672
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220

 cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act 720
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa		768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys		
245	250	255
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag		816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys		
260	265	270
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc		864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe		
275	280	285
aaa gga aaa taa		876
Lys Gly Lys		
290		
<210> 9		
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<212> PRT		
<213> Campylobacter jejuni		
<220>		
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II		
(CstII) from C. jejuni O:19		
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Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile		
1 5 10 15		
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln		
20 25 30		
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val		
35 40 45		
Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Leu Lys His		
50 55 60		
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn		
65 70 75 80		
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr		
85 90 95		
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu		
100 105 110		
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln		
115 120 125		
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly		
130 135 140		
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser		
145 150 155 160		
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro		
165 170 175		
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr		
180 185 190		
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu		
195 200 205		
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala		
210 215 220		
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr		
225 230 235 240		
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys		
245 250 255		
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys		
260 265 270		

Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
275 280 285
Lys Gly Lys
290

<210> 10
<211> 294
<212> PRT
<213> Campylobacter jejuni

<220>
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni strain NCTC 11168

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1 5 10 15
Lys Asn Ile Asp Tyr Lys Arg Leu Pro Lys Gln Phe Asp Val Phe Arg
20 25 30
Cys Asn Gln Phe Tyr Phe Glu Asp Arg Tyr Phe Val Gly Lys Asp Val
35 40 45
Lys Tyr Val Phe Phe Asn Pro Phe Val Phe Glu Gln Tyr Tyr Thr
50 55 60
Ser Lys Lys Leu Ile Gln Asn Glu Glu Tyr Asn Ile Glu Asn Ile Val
65 70 75 80
Cys Ser Thr Ile Asn Leu Glu Tyr Ile Asp Gly Phe Gln Phe Val Asp
85 90 95
Asn Phe Glu Leu Tyr Phe Ser Asp Ala Phe Leu Gly His Glu Ile Ile
100 105 110
Lys Lys Leu Lys Asp Phe Phe Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr
115 120 125
Asn Arg Gln Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Thr Ala Val
130 135 140
Ala Leu Gly Tyr Lys Ser Ile Tyr Ile Ser Gly Ile Asp Phe Tyr Gln
145 150 155 160
Asp Thr Asn Asn Leu Tyr Ala Phe Asp Asn Asn Lys Lys Asn Leu Leu
165 170 175
Asn Lys Cys Thr Gly Phe Lys Asn Gln Lys Phe Lys Phe Ile Asn His
180 185 190
Ser Met Ala Cys Asp Leu Gln Ala Leu Asp Tyr Leu Met Lys Arg Tyr
195 200 205
Asp Val Asn Ile Tyr Ser Leu Asn Ser Asp Glu Tyr Phe Lys Leu Ala
210 215 220
Pro Asp Ile Gly Ser Asp Phe Val Leu Ser Lys Lys Pro Lys Lys Tyr
225 230 235 240
Ile Asn Asp Ile Leu Ile Pro Asp Lys Tyr Ala Gln Glu Arg Tyr Tyr
245 250 255
Gly Lys Lys Ser Arg Leu Lys Glu Asn Leu His Tyr Lys Leu Ile Lys
260 265 270
Asp Leu Ile Arg Leu Pro Ser Asp Ile Lys His Tyr Leu Lys Glu Lys
275 280 285
Tyr Ala Asn Lys Asn Arg
290

<210> 11
<211> 873
<212> DNA
<213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(873)
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:4

<400> 11

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Met	Lys	Lys	Val	Ile	Ile	Ala	Gly	Asn	Gly	Pro	Ser	Leu	Lys	Glu	Ile	
1			5							10				15		

gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa

Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln	96
20								25					30			

ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg

Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Ala	Val	144
35							40					45				

ttt tac acc cct ggt ttc ttc ttt gag caa tac tac act tta aaa cat

Phe	Tyr	Thr	Pro	Gly	Phe	Phe	Glu	Gln	Tyr	Tyr	Thr	Leu	Lys	His	192
50							55				60				

tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat

Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn	240
65					70				75				80			

tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac

Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr	288
85								90					95			

gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt

Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu	336
100							105					110				

aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa

Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Phe	Asn	Gln	384
115							120					125				

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga

Arg	Ile	Thr	Ser	Gly	Val	Tyr	Met	Cys	Ala	Val	Ala	Ile	Ala	Leu	Gly	432
130					135					140						

tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca

Tyr	Lys	Glu	Ile	Tyr	Leu	Ser	Gly	Ile	Asp	Phe	Tyr	Gln	Asn	Gly	Ser	480
145					150				155			160				

tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct

Ser	Tyr	Ala	Phe	Asp	Thr	Lys	Gln	Glu	Asn	Leu	Leu	Lys	Leu	Ala	Pro	528
165								170					175			

gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca

Asp	Phe	Lys	Asn	Asp	Arg	Ser	His	Tyr	Ile	Gly	His	Ser	Lys	Asn	Thr	576
180								185					190			

gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta

Asp	Ile	Lys	Ala	Leu	Glu	Phe	Leu	Glu	Lys	Thr	Tyr	Lys	Ile	Lys	Leu	624
195								200					205			

tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210	215
220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225	230
235	240
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245	250
255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260	265
270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275	280
285	
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 12
<211> 291
<212> PRT
<213> *Campylobacter jejuni*

<220>
<223> *Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II*
(CstII) from *C. jejuni* O:4

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Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
1 5 10 15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
20 25 30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
35 40 45
Phe Tyr Thr Pro Gly Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
50 55 60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
65 70 75 80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
85 90 95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
100 105 110
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
115 120 125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130 135 140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
145 150 155 160
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
165 170 175
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
180 185 190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
195 200 205

Tyr	Cys	Leu	Cys	Pro	Asn	Ser	Leu	Leu	Ala	Asn	Phe	Ile	Glu	Leu	Ala
210							215					220			
Pro	Asn	Leu	Asn	Ser	Asn	Phe	Ile	Ile	Gln	Glu	Lys	Asn	Asn	Tyr	Thr
225							230				235				240
Lys	Asp	Ile	Leu	Ile	Pro	Ser	Ser	Glu	Ala	Tyr	Gly	Lys	Phe	Ser	Lys
							245				250				255
Asn	Ile	Asn	Phe	Lys	Lys	Ile	Lys	Glu	Asn	Val	Tyr	Tyr	Tyr	Lys	
							260				265				270
Leu	Ile	Lys	Asp	Leu	Leu	Arg	Leu	Pro	Ser	Asp	Ile	Lys	His	Tyr	Phe
							275				280				285
Lys	Gly	Lys													
			290												

<210> 13
<211> 873
<212> DNA
<213> *Campylobacter jejuni*

<220>
<221> CDS
<222> (1)..(873)
<223> *Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II*
(CstII) from *C. jejuni* O:36

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1			5							10					15
gat	tat	tca	agg	cta	cca	aat	gat	ttt	gat	gta	ttt	aga	tgt	aat	caa
Asp	Tyr	Ser	Arg	Leu	Pro	Asn	Asp	Phe	Asp	Val	Phe	Arg	Cys	Asn	Gln
			20							25					30
ttt	tat	ttt	gaa	gat	aaa	tac	tat	ctt	ggt	aaa	aaa	tgc	aaa	aca	gtg
Phe	Tyr	Phe	Glu	Asp	Lys	Tyr	Tyr	Leu	Gly	Lys	Lys	Cys	Lys	Thr	Val
			35					40				45			
ttt	tac	acc	cct	aat	ttc	ttc	ttt	gag	caa	tac	tac	act	tta	aaa	cat
Phe	Tyr	Thr	Pro	Asn	Phe	Phe	Glu	Gln	Tyr	Tyr	Leu	Lys	His		
			50					55			60				
tta	atc	caa	aat	caa	gaa	tat	gag	acc	cta	att	atg	tgt	tct	aat	
Leu	Ile	Gln	Asn	Gln	Glu	Tyr	Glu	Thr	Glu	Leu	Ile	Met	Cys	Ser	Asn
			65					70			75				80
tac	aac	caa	gct	cat	cta	gaa	aat	gaa	aat	ttt	gta	aaa	act	ttt	tac
Tyr	Asn	Gln	Ala	His	Leu	Glu	Asn	Glu	Asn	Phe	Val	Lys	Thr	Phe	Tyr
			85							90			95		
gat	tat	ttt	cct	gat	gct	cat	ttg	gga	tat	gat	ttt	ttt	aaa	caa	ctt
Asp	Tyr	Phe	Pro	Asp	Ala	His	Leu	Gly	Tyr	Asp	Phe	Phe	Lys	Gln	Leu
			100						105			110			
aaa	gaa	ttt	aat	gct	tat	ttt	aaa	ttt	cac	gaa	att	tat	ttc	aat	caa
Lys	Glu	Phe	Asn	Ala	Tyr	Phe	Lys	Phe	His	Glu	Ile	Tyr	Phe	Asn	Gln
			115						120			125			

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130	135
	140
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145	150
	155
	160
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165	170
	175
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180	185
	190
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195	200
	205
tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210	215
	220
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225	230
	235
	240
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245	250
	255
aat att aat ttt aaa aat aat aat att aat gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260	265
	270
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275	280
	285
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 14

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:36

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1	5
	10
	15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20	25
	30

Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val
 35 40 45
 Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 15

<211> 1170

<212> DNA

<213> Campylobacter jejuni

<220>

<223> glycosyltransferase from C. jejuni strain OH4384
 (ORF 4a of lipooligosaccharide (LOS) biosynthesis
 locus)

<400> 15

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 ttatcatcg ttatcaatca aacttatact aacttagaaa tcatacttgt caatgatgg 120
 agcacagatg aacactcact caatattgca aaagaatata ccttaaaaga taaaagaata 180
 actcttttg ataagaaaaa tgggggttta agttcagcta gaaatatagg tatagaatac 240
 tttagcgggg aatataaatt aaaaaacaaa actcaacata taaaagaaaa ttctttaata 300
 gaatttcaat tggatggtaa taatccttat aatatatata aagcatataa aagctctcaa 360
 gctttaata atgaaaaaaga tttaaccaat ttacttacc ctatgtataga ttatattata 420
 ttcttagata gtgataatta ttggaaacta aactgcata gaaatgcgt tataagaatg 480
 aaaaatgtgg atgtattgtg gtttgaccat gattgcacct atgaagacaa tataaaaaat 540
 aagcacaaaaa aaacaaggat ggaaattttt gatTTaaaaa aagaatgtat aatcactcca 600
 aaagaatatg caaatcgagc attaagtgtt ggtatctagag atatTTTTT tggatggat 660
 ggaatgattt gatTTTTT ttggaaactt aattaaactt aatttataaa ttttattatc 720
 aatgaagata tacactttgg gataattttt tttgcttagt gtaataaaat ttatgtttt 780
 tcacaaaaagt tgtatttgg tcgtttaaga gcaaacagta tatcaaatca tgataagaag 840

attacaaaag	caaatgtgtc	agagtatttt	aaagatatat	atgaaaacttt	cggggaaaac	900
gctaagaag	caaaaaatta	ttaaaaagca	gcaaggcagg	ttataactgc	tttaaaaattg	960
atagaatttt	ttaaagatca	aaaaaacgaa	aatgcacctg	ctataaaaga	aacattttt	1020
ccttgctatg	ccaaaaaaagc	ttaatgatt	aaaaaaattt	aaaaagatcc	tttaaattt	1080
aaggaacaat	tagtttaat	taaacctttt	attcaaacaa	aacttcctta	tgatatttgg	1140
aaattttggc	aaaaaataaa	aaatattttaa				1170

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<210> 16
<211> 1044
<212> DNA
<213> Campylobacter jejuni
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<220>
<221> CDS
<222> (1)..(1044)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni strain OH4384 (ORF 5a
of lipoooligosaccharide (LOS) biosynthesis locus)

<400> 16
atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
1 5 10 15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
 Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
 20 25 30

ata caa cga gat aaa atc gat tct tat tta cca aaa aaa act ctt gtg	144	
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val		
35	40	45

caa attaataaa tac aac aat gaa gat tta att aaa ctt aat aaa gct 192
 Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
 50 55 60

att ata ggg gag ggg cat aaa gga tat ttt aat tat tat gat gaa aaa tct 240
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
65 70 75 80

aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa 288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
85 90 95

aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct 336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
100 105 110

atc caa aga ggt gtt ata gga tat aat gat tgt acc gat gga agt gaa 384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
115 120 125

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gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata    432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
   130           135           140

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aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat 480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
145 150 155 160

aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165	170
	175
gag tgg ctt ata aaa ata gat gtg gat cat atc tat gat gct aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys	
180	185
	190
ctt tat aaa agc ttc tat ata cca aaa aac aaa tat gat gta gtt agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser	
195	200
	205
tat tca agg gtt gat att cac tat ttt aat gat aat ttt ttt ctt tgt	672
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys	
210	215
	220
aaa gat aat aat ggc aat ata ttg aaa gaa cca gga gat tgc ttg ctt	720
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu	
225	230
	235
	240
atc aat aat tat aac tta aaa tgg aaa gaa gta tta att gac aga atc	768
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile	
245	250
	255
aat aac aat tgg aaa aaa gca aca aaa caa agt ttt tct tca aat ata	816
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile	
260	265
	270
cac tct tta gag caa tta aag tat aaa cac agg ata tta ttt cac act	864
His Ser Ile Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr	
275	280
	285
gaa tta aat aat tat cat ttt cct ttt tta aaa aaa cat aga gct caa	912
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln	
290	295
	300
gat att tat aaa tat aat tgg ata agt att gaa gaa ttt aaa aaa ttc	960
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe	
305	310
	315
	320
tat tta caa aat att aat cat aaa ata gaa cct tct atg att tca aaa	1008
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys	
325	330
	335
gaa act cta aaa aaa ata ttc tta aca ttg ttt taa	1044
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe	
340	345
<210> 17	
<211> 347	
<212> PRT	
<213> <i>Campylobacter jejuni</i>	
<220>	
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)	
transferase from <i>C. jejuni</i> strain OH4384 (ORF 5a	
of lipooligosaccharide (LOS) biosynthesis locus)	

<400> 17

Met	Leu	Phe	Gln	Ser	Tyr	Phe	Val	Lys	Ile	Ile	Cys	Leu	Phe	Ile	Pro
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Phe	Arg	Lys	Ile	Arg	His	Lys	Ile	Lys	Thr	Phe	Leu	Leu	Lys	Asn	
					20			25						30	
Ile	Gln	Arg	Asp	Lys	Ile	Asp	Ser	Tyr	Leu	Pro	Lys	Lys	Thr	Leu	Val
					35			40						45	
Gln	Ile	Asn	Lys	Tyr	Asn	Asn	Glu	Asp	Leu	Ile	Lys	Leu	Asn	Lys	Ala
					50			55			60				
Ile	Ile	Gly	Glu	Gly	His	Lys	Gly	Tyr	Phe	Asn	Tyr	Asp	Glu	Lys	Ser
					65			70			75			80	
Lys	Asp	Pro	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Ala	Phe	Ile	Arg	Val	Lys
					85				90					95	
Asn	Glu	Ala	Ile	Thr	Leu	Lys	Ala	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala
					100				105					110	
Ile	Gln	Arg	Gly	Val	Ile	Gly	Tyr	Asn	Asp	Cys	Thr	Asp	Gly	Ser	Glu
					115			120						125	
Glu	Ile	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Ser	Phe	Ile	Pro	Ile
					130			135					140		
Lys	Tyr	Pro	Tyr	Glu	Ile	Gln	Ile	Gln	Asn	Pro	Lys	Ser	Glu	Glu	Asn
					145			150			155			160	
Lys	Leu	Tyr	Ser	Tyr	Tyr	Asn	Tyr	Val	Ala	Ser	Phe	Ile	Pro	Lys	Asp
					165				170					175	
Glu	Trp	Leu	Ile	Lys	Ile	Asp	Val	Asp	His	Ile	Tyr	Asp	Ala	Lys	Lys
					180			185					190		
Leu	Tyr	Lys	Ser	Phe	Tyr	Ile	Pro	Lys	Asn	Lys	Tyr	Asp	Val	Val	Ser
					195			200					205		
Tyr	Ser	Arg	Val	Asp	Ile	His	Tyr	Phe	Asn	Asp	Asn	Phe	Phe	Leu	Cys
					210			215					220		
Lys	Asp	Asn	Asn	Gly	Asn	Ile	Leu	Lys	Glu	Pro	Gly	Asp	Cys	Leu	Leu
					225			230			235			240	
Ile	Asn	Asn	Tyr	Asn	Leu	Lys	Trp	Lys	Glu	Val	Leu	Ile	Asp	Arg	Ile
					245				250					255	
Asn	Asn	Asn	Trp	Lys	Lys	Ala	Thr	Lys	Gln	Ser	Phe	Ser	Ser	Asn	Ile
					260				265					270	
His	Ser	Leu	Glu	Gln	Leu	Lys	Tyr	Lys	His	Arg	Ile	Leu	Phe	His	Thr
					275			280					285		
Glu	Leu	Asn	Asn	Tyr	His	Phe	Pro	Phe	Leu	Lys	Lys	His	Arg	Ala	Gln
					290			295			300				
Asp	Ile	Tyr	Lys	Tyr	Asn	Trp	Ile	Ser	Ile	Glu	Glu	Phe	Lys	Lys	Phe
					305			310			315			320	
Tyr	Leu	Gln	Asn	Ile	Asn	His	Lys	Ile	Glu	Pro	Ser	Met	Ile	Ser	Lys
					325				330					335	
Glu	Thr	Leu	Lys	Ile	Phe	Leu	Thr	Leu	Phe						
					340			345							

<210> 18
<211> 1608
<212> DNA
<213> *Campylobacter jejuni*

<220>
<221> CDS
<222> (1)..(1608)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from *C. jejuni* O:1

<400> 18				
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Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile				
1 5 10 15				
gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa				96
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys				
20 25 30				
aaa atc tac aat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac				144
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn				
35 40 45				
tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta				192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val				
50 55 60				
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct				240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro				
65 70 75 80				
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt				288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser				
85 90 95				
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca				336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro				
100 105 110				
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa				384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu				
115 120 125				
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa				432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln				
130 135 140				
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa				480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys				
145 150 155 160				
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga				528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg				
165 170 175				
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat				576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn				
180 185 190				
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa				624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln				
195 200 205				
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag				672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln				
210 215 220				
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa				720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln				
225 230 235 240				

att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp 245	250	255	768	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu 260	265	270	816	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg 275	280	285	864	
aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg 290	295	300	912	
gaa ata tta gat aaa ttg aaa ttg agt ggt aaa aaa atg act tta gct Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala 305	310	315	320	960
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu 325	330	335	1008	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala 340	345	350	1056	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp 355	360	365	1104	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg 370	375	380	1152	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu 385	390	395	400	1200
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln 405	410	415	1248	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu 420	425	430	1296	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys 435	440	445	1344	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys 450	455	460	1392	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro 465	470	475	480	1440

aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta		1488	
Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu			
485	490	495	
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata		1536	
Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile			
500	505	510	
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa		1584	
Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys			
515	520	525	
aga gtt aat aat ata agc ttc tta		1608	
Arg Val Asn Asn Ile Ser Phe Leu			
530	535		
<210> 19			
<211> 536			
<212> PRT			
<213> Campylobacter jejuni			
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc) transferase from C. jejuni O:1			
<400> 19			
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1	5	10	15
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys			
20	25	30	
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn			
35	40	45	
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val			
50	55	60	
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro			
65	70	75	80
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser			
85	90	95	
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro			
100	105	110	
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu			
115	120	125	
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln			
130	135	140	
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys			
145	150	155	160
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg			
165	170	175	
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn			
180	185	190	
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln			
195	200	205	
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln			
210	215	220	
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln			
225	230	235	240
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp			
245	250	255	
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu			
260	265	270	

Asp	Ala	Leu	Thr	Leu	Glu	Asp	Phe	Lys	Lys	Ile	His	Tyr	Arg	His	Arg
							275	280				285			
Lys	Ile	Lys	Lys	Ile	Asn	Tyr	Thr	Met	Leu	Asp	Glu	Lys	Val	Ile	Arg
							290	295				300			
Glu	Ile	Leu	Asp	Lys	Phe	Lys	Leu	Ser	Gly	Lys	Lys	Met	Thr	Leu	Ala
							305	310				315			320
Ile	Ile	Pro	Ala	Arg	Ala	Gly	Ser	Lys	Gly	Ile	Lys	Asn	Lys	Asn	Leu
							325					330			335
Ala	Leu	Leu	His	Asp	Arg	Pro	Leu	Leu	Tyr	Tyr	Thr	Ile	Asn	Ala	Ala
							340					345			350
Lys	Asn	Ser	Lys	Tyr	Val	Asp	Lys	Ile	Val	Leu	Ser	Ser	Asp	Gly	Asp
							355					360			365
Asp	Ile	Leu	Glu	Tyr	Gly	Gln	Thr	Gln	Gly	Val	Asp	Val	Leu	Lys	Arg
							370	375				380			
Pro	Lys	Glu	Leu	Ala	Leu	Asp	Asp	Thr	Thr	Ser	Asp	Lys	Val	Val	Leu
							385	390				395			400
His	Thr	Leu	Ser	Phe	Tyr	Lys	Asp	Tyr	Glu	Asn	Ile	Val	Leu	Leu	Gln
							405					410			415
Pro	Thr	Ser	Pro	Leu	Arg	Thr	Asn	Val	His	Ile	Asp	Glu	Ala	Phe	Leu
							420					425			430
Lys	Phe	Lys	Asn	Glu	Asn	Ser	Asn	Ala	Leu	Ile	Ser	Val	Val	Glu	Cys
							435					440			445
Asp	Asn	Lys	Ile	Leu	Lys	Ala	Phe	Ile	Asp	Asp	Asn	Gly	Asn	Leu	Lys
							450					455			460
Gly	Ile	Cys	Asp	Asn	Lys	Tyr	Pro	Phe	Met	Pro	Arg	Gln	Lys	Leu	Pro
							465					470			480
Lys	Thr	Tyr	Met	Ser	Asn	Gly	Ala	Ile	Tyr	Ile	Val	Lys	Ser	Asn	Leu
							485					490			495
Phe	Leu	Asn	Asn	Pro	Thr	Phe	Leu	Gln	Glu	Lys	Thr	Ser	Cys	Tyr	Ile
							500					505			510
Met	Asp	Glu	Lys	Ala	Ser	Leu	Asp	Ile	Asp	Thr	Thr	Glu	Asp	Leu	Lys
							515					520			525
Arg	Val	Asn	Asn	Ile	Ser	Phe	Leu								
							530					535			

<210> 20
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<212> DNA
<213> *Campylobacter jejuni*

<220>
<221> CDS
<222> (1)..(1056)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from *C. jejuni* O:10

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Met	Leu	Phe	Gln	Ser	Tyr	Phe	Val	Lys	Ile	Ile	Cys	Leu	Phe	Ile	Pro	
1		5								10					15	
ttt	aga	aaa	att	aga	cat	aaa	ata	aaa	aaa	aca	ttt	tta	cta	aaa	aac	96
Phe	Arg	Lys	Ile	Arg	His	Lys	Ile	Lys	Lys	Thr	Phe	Leu	Leu	Lys	Asn	
												20		25		30
ata	caa	cga	gat	aaa	atc	gat	tct	tat	cta	cca	aaa	aaa	act	ctt	ata	144
Ile	Gln	Arg	Asp	Lys	Ile	Asp	Ser	Tyr	Leu	Pro	Lys	Lys	Thr	Leu	Ile	
												35		40		45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	192
50 55 60	
att ata ggg ggg ggg cat aaa gga tat ttt aat tat gat gaa aaa tct Ile Ile Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	240
65 70 75 80	
aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	288
85 90 95	
aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	336
100 105 110	
att caa aga ggt gtt ata gga tat aat gat tgc acc gat gga agt gaa Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	384
115 120 125	
gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	432
130 135 140	
aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	480
145 150 155 160	
aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	528
165 170 175	
gag tgg ctc ata aaa ata gat gtg gat cat tat tat gat gca aaa aaa Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	576
180 185 190	
tta tat aag agt ttt tat ata cct aga aaa aat tat cat gta att agt Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	624
195 200 205	
tac tct agg ata gat ttt ata ttt aat gaa gaa aaa ttt tat gtt tat Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	672
210 215 220	
cgg aat aag gag ggg gag att tta aaa gct cct gga gat tgt tta gca Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	720
225 230 235 240	
ata caa aac act aac tta ttt tgg aaa gaa ata ctt att gaa gat gat Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	768
245 250 255	
aca ttt aag tgg aat act gca aaa aat aat ata gag aat gca aaa tca Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	816
260 265 270	
tat gaa att tta aaa gtt aga aat aga att tat ttt act aca gaa ctt Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu	864
275 280 285	

aat aat tat cat ttt cca ttt ata aaa aat tat aga aaa aat gat tat	912
Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr	
290	295
295	300
 aag cag tta aat tgg gtt agc tta gat gat ttt att aaa aat tat aaa	960
Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys	
305	310
310	315
315	320
 gaa aaa tta aaa aat caa ata gat ttt aaa atg cta gaa tac aaa aca	1008
Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr	
325	330
330	335
 tta aaa aaa gtg tac aaa aag ctt aca tct tca gca agc gat aaa att	1056
Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile	
340	345
345	350
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transferase from C. jejuni O:10	
 <400> 21	
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro	
1	5
5	10
10	15
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn	
20	25
25	30
30	
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile	
35	40
40	45
45	
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50	55
55	60
60	
Ile Ile Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65	70
70	75
75	80
80	
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85	90
90	95
95	
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100	105
105	110
110	
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115	120
120	125
125	
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130	135
135	140
140	
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145	150
150	155
155	160
160	
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165	170
170	175
175	
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180	185
185	190
190	
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195	200
200	205
205	
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210	215
215	220
220	
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225	230
230	235
235	240
240	
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245	250
250	255
255	
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260	265
265	270
270	

Tyr	Glu	Ile	Leu	Lys	Val	Arg	Asn	Arg	Ile	Tyr	Phe	Thr	Thr	Glu	Leu
275					280						285				
Asn	Asn	Tyr	His	Phe	Pro	Phe	Ile	Lys	Asn	Tyr	Arg	Lys	Asn	Asp	Tyr
290					295						300				
Lys	Gln	Leu	Asn	Trp	Val	Ser	Leu	Asp	Asp	Phe	Ile	Lys	Asn	Tyr	Lys
305					310					315					320
Glu	Lys	Leu	Lys	Asn	Gln	Ile	Asp	Phe	Lys	Met	Leu	Glu	Tyr	Lys	Thr
						325			330						335
Leu	Lys	Lys	Val	Tyr	Lys	Lys	Leu	Thr	Ser	Ser	Ala	Ser	Asp	Lys	Ile
							340		345						350

<210> 22
<211> 945
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(945)
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:36

<400>	22															
atg	ctt	aaa	aaa	atc	att	tct	tta	tat	aaa	aga	tac	tcg	att	tct	aaa	48
Met		Leu	Lys	Ile	Ile	Ser	Leu	Tyr	Lys	Arg	Tyr	Ser	Ile	Ser	Lys	
1		5					10						15			
aaa	ttg	gtt	tta	gat	aat	gag	cat	ttc	att	aag	gaa	aat	aaa	aac	atc	96
Lys	Leu	Val	Leu	Asp	Asn	Glu	His	Phe	Ile	Lys	Glu	Asn	Lys	Asn	Ile	
		20					25						30			
tat	gga	aaa	aaa	cat	aag	ggc	ttt	ttt	gac	ttt	gat	gaa	aag	gct	aag	144
Tyr	Gly	Lys	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Glu	Lys	Ala	Lys	
		35					40					45				
gat	gtg	aaa	tca	ccc	ctt	aat	cct	tgg	gga	ttt	atc	agg	gtt	aaa	aat	192
Asp	Val	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Gly	Phe	Ile	Arg	Val	Lys	Asn	
		50			55			60								
gaa	gct	tta	acc	cta	aga	gtt	tct	tta	gaa	agt	ata	cta	cct	gct	tta	240
Glu	Ala	Leu	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala	Leu	
		65			70			75					80			
caa	aga	gga	att	ata	gct	tac	aac	gac	tgt	gat	gat	ggg	agt	gaa	gag	288
Gln	Arg	Gly	Ile	Ile	Ala	Tyr	Asn	Asp	Cys	Asp	Asp	Gly	Ser	Glu	Glu	
		85			90							95				
ctt	att	tta	gaa	ttt	tgc	aag	caa	tat	ccc	aac	ttc	att	gct	aaa	aaa	336
Leu	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Asn	Phe	Ile	Ala	Lys	Lys	
		100			105			110								
tat	cct	tat	aaa	gta	gat	cta	gaa	aat	cct	aaa	aat	gaa	aat	aaa		384
Tyr	Pro	Tyr	Lys	Val	Asp	Leu	Glu	Asn	Pro	Lys	Asn	Glu	Glu	Asn	Lys	
		115			120			125								
ctt	tac	tct	tat	tac	aat	tgg	gca	gca	tct	ttt	ata	ccc	tta	gat	gag	432
Leu	Tyr	Ser	Tyr	Tyr	Asn	Trp	Ala	Ala	Ser	Phe	Ile	Pro	Leu	Asp	Glu	
		130			135						140					

tgg ttt ata aaa atc gat gtg gat cat tac tac gat gcc aag aag ctt	480
Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu	
145 150 155 160	
tat aag agt ttt tat agg att gat caa gaa aat aaa gcc tta tgc tac	528
Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr	
165 170 175	
cca aga att aat ttt ata atc tta aat gga aat att tat gtg caa aat	576
Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn	
180 185 190	
agt gga aat tat gga ttc ata ggg ggg ggg gat caa ctc ttg att aaa	624
Ser Gly Asn Tyr Gly Phe Ile Gly Gly Asp Gln Leu Leu Ile Lys	
195 200 205	
aga aga aat agt agc ttt ata gaa aga agg gtt tca aaa aaa agc caa	672
Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln	
210 215 220	
tgg ata gat cct aag gga ctt ata gaa gaa ctc tac tcc gag caa caa	720
Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
gtc tta tct caa gga gtg aaa ata cta caa gct ccc cta ctt cag tgg	768
Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp	
245 250 255	
cat ttt cct gcc tta aaa tac cgc cga aac gat tac caa caa tat tta	816
His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu	
260 265 270	
gat atc ttg agt tta gaa gaa ttt cag gcc ttt cat cgt aag agc aaa	864
Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys	
275 280 285	
gag gct aaa aaa ata gac ttt gcc atg cta aaa cgc cct gta atc gag	912
Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu	
290 295 300	
caa ata tta aag aaa ttt caa gga gag ata aaa	945
Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys	
305 310 315	
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<211> 315	
<212> PRT	
<213> <i>Campylobacter jejuni</i>	
<220>	
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)	
transferase from <i>C. jejuni</i> O:36	
<400> 23	
Met Leu Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys	
1 5 10 15	
Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile	
20 25 30	
Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys	
35 40 45	

Asp	Val	Lys	Ser	Pro	Leu	Asn	Pro	Trp	Gly	Phe	Ile	Arg	Val	Lys	Asn
50															60
Glu	Ala	Leu	Thr	Leu	Arg	Val	Ser	Leu	Glu	Ser	Ile	Leu	Pro	Ala	Leu
65															80
Gln	Arg	Gly	Ile	Ile	Ala	Tyr	Asn	Asp	Cys	Asp	Asp	Gly	Ser	Glu	Glu
															95
Leu	Ile	Leu	Glu	Phe	Cys	Lys	Gln	Tyr	Pro	Asn	Phe	Ile	Ala	Lys	Lys
															100
Tyr	Pro	Tyr	Lys	Val	Asp	Leu	Glu	Asn	Pro	Lys	Asn	Glu	Glu	Asn	Lys
															110
Leu	Tyr	Ser	Tyr	Tyr	Asn	Trp	Ala	Ala	Ser	Phe	Ile	Pro	Leu	Asp	Glu
															125
Trp	Phe	Ile	Lys	Ile	Asp	Val	Asp	His	Tyr	Tyr	Asp	Ala	Lys	Lys	Leu
145															160
Tyr	Lys	Ser	Phe	Tyr	Arg	Ile	Asp	Gln	Glu	Asn	Lys	Ala	Leu	Cys	Tyr
															175
Pro	Arg	Ile	Asn	Phe	Ile	Ile	Leu	Asn	Gly	Asn	Ile	Tyr	Val	Gln	Asn
															190
Ser	Gly	Asn	Tyr	Gly	Phe	Ile	Gly	Gly	Gly	Asp	Gln	Leu	Leu	Ile	Lys
															205
Arg	Arg	Asn	Ser	Ser	Phe	Ile	Glu	Arg	Arg	Val	Ser	Lys	Lys	Ser	Gln
															220
Trp	Ile	Asp	Pro	Lys	Gly	Leu	Ile	Glu	Glu	Leu	Tyr	Ser	Glu	Gln	Gln
225															240
Val	Leu	Ser	Gln	Gly	Val	Lys	Ile	Leu	Gln	Ala	Pro	Leu	Leu	Gln	Trp
															255
His	Phe	Pro	Ala	Leu	Lys	Tyr	Arg	Arg	Asn	Asp	Tyr	Gln	Gln	Tyr	Leu
															270
Asp	Ile	Leu	Ser	Leu	Glu	Glu	Phe	Gln	Ala	Phe	His	Arg	Lys	Ser	Lys
															285
Glu	Ala	Lys	Lys	Ile	Asp	Phe	Ala	Met	Leu	Lys	Arg	Pro	Val	Ile	Glu
															300
Gln	Ile	Leu	Lys	Lys	Phe	Gln	Gly	Glu	Ile	Lys					
															315

<210> 24
 <211> 1608
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(1608)
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni NCTC 11168

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Met	Thr	Leu	Phe	Tyr	Lys	Ile	Ile	Ala	Phe	Leu	Arg	Leu	Leu	Lys	Ile	
1															15	
gat	aaa	aaa	tta	aaa	ttt	gat	aat	gaa	tat	ttt	tta	aac	tta	aat	aaa	96
Asp	Lys	Lys	Leu	Lys	Phe	Asp	Asn	Glu	Tyr	Phe	Leu	Asn	Leu	Asn	Lys	
															20	
															25	
															30	
aaa	atc	tac	gat	gaa	aag	cat	aaa	ggg	ttt	ttt	gat	ttt	gat	cca	aac	144
Lys	Ile	Tyr	Asp	Glu	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Pro	Asn	
															35	
															40	
															45	

tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	192
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	240
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	288
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	336
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	384
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	432
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	480
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	528
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	576
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	624
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	672
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	720
225 230 235 240	
att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	768
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	816
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	864
275 280 285	

aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg 290 295 300	912
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala 305 310 315 320	960
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu 325 330 335	1008
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala 340 345 350	1056
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp 355 360 365	1104
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg 370 375 380	1152
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu 385 390 395 400	1200
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln 405 410 415	1248
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu 420 425 430	1296
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys 435 440 445	1344
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys 450 455 460	1392
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro 465 470 475 480	1440
aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu 485 490 495	1488
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile 500 505 510	1536
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys 515 520 525	1584

aga gtt aat aat ata agc ttc tta
Arg Val Asn Asn Ile Ser Phe Leu
530 535

1608

<210> 25
<211> 536
<212> PRT
<213> Campylobacter jejuni

<220>
<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni NCTC 11168

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Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
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Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
20 25 30
Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
35 40 45
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val
50 55 60
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro
65 70 75 80
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser
85 90 95
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro
100 105 110
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu
115 120 125
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln
130 135 140
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys
145 150 155 160
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg
165 170 175
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn
180 185 190
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln
195 200 205
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln
210 215 220
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln
225 230 235 240
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp
245 250 255
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu
260 265 270
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg
275 280 285
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg
290 295 300
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala
305 310 315 320
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu
325 330 335
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala
340 345 350
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp
355 360 365

Asp	Ile	Leu	Glu	Tyr	Gly	Gln	Thr	Gln	Gly	Val	Asp	Val	Leu	Lys	Arg
370					375					380					
Pro	Lys	Glu	Leu	Ala	Leu	Asp	Asp	Thr	Thr	Ser	Asp	Lys	Val	Val	Leu
385					390					395					400
His	Thr	Leu	Ser	Phe	Tyr	Lys	Asp	Tyr	Glu	Asn	Ile	Val	Leu	Leu	Gln
					405				410					415	
Pro	Thr	Ser	Pro	Leu	Arg	Thr	Asn	Val	His	Ile	Asp	Glu	Ala	Phe	Leu
					420			425				430			
Lys	Phe	Lys	Asn	Glu	Asn	Ser	Asn	Ala	Leu	Ile	Ser	Val	Val	Glu	Cys
					435			440				445			
Asp	Asn	Lys	Ile	Leu	Lys	Ala	Phe	Ile	Asp	Asp	Asn	Gly	Asn	Leu	Lys
					450			455			460				
Gly	Ile	Cys	Asp	Asn	Lys	Tyr	Pro	Phe	Met	Pro	Arg	Gln	Lys	Leu	Pro
					465			470		475					480
Lys	Thr	Tyr	Met	Ser	Asn	Gly	Ala	Ile	Tyr	Ile	Val	Lys	Ser	Asn	Leu
					485			490			495				
Phe	Leu	Asn	Asn	Pro	Thr	Phe	Leu	Gln	Glu	Lys	Thr	Ser	Cys	Tyr	Ile
					500			505			510				
Met	Asp	Glu	Lys	Ala	Ser	Leu	Asp	Ile	Asp	Thr	Thr	Glu	Asp	Leu	Lys
					515			520			525				
Arg	Val	Asn	Asn	Ile	Ser	Phe	Leu								
					530			535							

<210> 26
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<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(906)
<223> beta-1,3-galactosyltransferase from C. jejuni strain
OH4384 (ORF 6a of lipooligosaccharide (LOS)
biosynthesis locus)

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Met	Phe	Lys	Ile	Ser	Ile	Ile	Leu	Pro	Thr	Tyr	Asn	Val	Glu	Gln	Tyr
1			5				10					15			
ata	gca	agg	gca	ata	gaa	agc	tgt	atc	aat	cag	act	ttt	aaa	gat	ata
Ile	Ala	Arg	Ala	Ile	Glu	Ser	Cys	Ile	Asn	Gln	Thr	Phe	Lys	Asp	Ile
				20			25				30				
gaa	ata	att	gta	gtt	gat	gat	tgt	gga	aat	gat	aat	agt	ata	aat	ata
Glu	Ile	Ile	Val	Val	Asp	Asp	Cys	Gly	Asn	Asp	Asn	Ser	Ile	Asn	Ile
				35			40				45				
gcc	aaa	gaa	tac	tct	aaa	aaa	gac	aaa	aga	ata	aaa	ata	atc	cac	aat
Ala	Lys	Glu	Tyr	Ser	Lys	Lys	Asp	Lys	Arg	Ile	Lys	Ile	Ile	His	Asn
				50			55			60					
gaa	aaa	aac	tta	ggt	ctt	tta	aga	gca	aga	tat	gaa	ggt	gtg	aaa	gta
Glu	Lys	Asn	Leu	Gly	Leu	Leu	Arg	Ala	Arg	Tyr	Glu	Gly	Val	Lys	Val
				65			70			75			80		
gca	aac	tct	cct	tat	ata	atg	ttt	tta	gat	cct	gat	gat	tat	ttg	gaa
Ala	Asn	Ser	Pro	Tyr	Ile	Met	Phe	Leu	Asp	Pro	Asp	Asp	Tyr	Leu	Glu
				85			90			95					

ctt aat gct tgt gaa gag tgt ata aaa att tta gat gaa cag gat gaa	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu	
100 105 110	
gtt gat tta gtg ttt ttc aat gct att gtt gaa agt aat gtt att tca	384
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser	
115 120 125	
tat aaa aag ttt gac ttt aat tct ggt ttt tat agc aaa aaa gag ttt	432
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe	
130 135 140	
gta aaa aaa att att gca aag aaa aat tta tat tgg act atg tgg ggg	480
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly	
145 150 155 160	
aaa ctt ata aga aag aaa ttg tat tta gaa gct ttt gcg agt tta aga	528
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg	
165 170 175	
ctc gag aaa gat gtt aaa atc aat atg gct gaa gat gta ttg tta tat	576
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr	
180 185 190	
tat cca atg tta agt caa gct caa aaa ata gca tat atg aac tgt aat	624
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn	
195 200 205	
tta tat cat tac gtg cct aat aat aat tca att tgt aat act aag aat	672
Leu Tyr His Tyr Val Pro Asn Asn Ser Ile Cys Asn Thr Lys Asn	
210 215 220	
gaa gtg ctt gtt aaa aat aat att caa gag ttg cag ttg gtt tta aac	720
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn	
225 230 235 240	
tat tta agg caa aat tat att tta aac aag tat tgt agc gtt ctc tat	768
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr	
245 250 255	
gtg cta att aaa tat ttg cta tat att caa ata tat aaa ata aaa aga	816
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg	
260 265 270	
aca aaa tta atg gtt aca tta gct aaa ata aat att tta act tta	864
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu	
275 280 285	
aaa att tta ttt aaa tat aaa aaa ttt tta aaa caa tgt taa	906
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys	
290 295 300	

<210> 27
 <211> 301
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,3-galactosyltransferase from C. jejuni strain
 OH4384 (ORF 6a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 27

Met	Phe	Lys	Ile	Ser	Ile	Ile	Leu	Pro	Thr	Tyr	Asn	Val	Glu	Gln	Tyr
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Ile	Ala	Arg	Ala	Ile	Glu	Ser	Cys	Ile	Asn	Gln	Thr	Phe	Lys	Asp	Ile
					20				25					30	
Glu	Ile	Ile	Val	Val	Asp	Asp	Cys	Gly	Asn	Asp	Asn	Ser	Ile	Asn	Ile
					35				40					45	
Ala	Lys	Glu	Tyr	Ser	Lys	Lys	Asp	Lys	Arg	Ile	Lys	Ile	Ile	His	Asn
	50					55					60				
Glu	Lys	Asn	Leu	Gly	Leu	Leu	Arg	Ala	Arg	Tyr	Glu	Gly	Val	Lys	Val
	65					70					75				80
Ala	Asn	Ser	Pro	Tyr	Ile	Met	Phe	Leu	Asp	Pro	Asp	Asp	Tyr	Leu	Glu
						85					90				95
Leu	Asn	Ala	Cys	Glu	Glu	Cys	Ile	Lys	Ile	Leu	Asp	Glu	Gln	Asp	Glu
							100			105					110
Val	Asp	Leu	Val	Phe	Phe	Asn	Ala	Ile	Val	Glu	Ser	Asn	Val	Ile	Ser
							115			120					125
Tyr	Lys	Lys	Phe	Asp	Phe	Asn	Ser	Gly	Phe	Tyr	Ser	Lys	Lys	Glu	Phe
	130					135					140				
Val	Lys	Lys	Ile	Ile	Ala	Lys	Lys	Asn	Leu	Tyr	Trp	Thr	Met	Trp	Gly
	145					150					155				160
Lys	Leu	Ile	Arg	Lys	Lys	Leu	Tyr	Leu	Glu	Ala	Phe	Ala	Ser	Leu	Arg
					165				170					175	
Leu	Glu	Lys	Asp	Val	Lys	Ile	Asn	Met	Ala	Glu	Asp	Val	Leu	Leu	Tyr
						180				185					190
Tyr	Pro	Met	Leu	Ser	Gln	Ala	Gln	Lys	Ile	Ala	Tyr	Met	Asn	Cys	Asn
							195			200					205
Leu	Tyr	His	Tyr	Val	Pro	Asn	Asn	Asn	Ser	Ile	Cys	Asn	Thr	Lys	Asn
							210			215					220
Glu	Val	Leu	Val	Lys	Asn	Asn	Ile	Gln	Glu	Leu	Gln	Leu	Val	Leu	Asn
	225							230			235				240
Tyr	Leu	Arg	Gln	Asn	Tyr	Ile	Leu	Asn	Lys	Tyr	Cys	Ser	Val	Leu	Tyr
						245				250					255
Val	Leu	Ile	Lys	Tyr	Leu	Leu	Tyr	Ile	Gln	Ile	Tyr	Lys	Ile	Lys	Arg
							260			265					270
Thr	Lys	Leu	Met	Val	Thr	Leu	Leu	Ala	Lys	Ile	Asn	Ile	Leu	Thr	Leu
							275			280					285
Lys	Ile	Leu	Phe	Lys	Tyr	Lys	Lys	Phe	Leu	Lys	Gln	Cys			
						290			295			300			

<210> 28
 <211> 912
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(912)
 <223> Campylobacter glycosyltransferase B (CgtB) beta-1,3
 galactosyltransferase from C. jejuni serotype O:2
 (strain NCTC 11168)

<400> 28
 atg agtcaaatttccatcatacttaacttatatatgtggaaaaaat
 Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr
 1 5 10 15
 att gct aga gca tta gaa agt tgc att aac caa act ttt aaa gat ata
 Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
 20 25 30
 gaa atc att gta gta gat gat tgt ggt aat gat aaa agt ata gat ata
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile
 35 40 45
 gct aaa gag tat gct agt aaa gat gat aga ata aaa atc ata cat aat
 Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn
 50 55 60
 gaa gag aat tta aag ctt tta aga gca aga tat gaa ggt gct aaa gta
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val
 65 70 75 80
 gca act tca cct tat atc atg ttt tta gat tct gat gat tat tta gaa
 Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu
 85 90 95
 ctt aat gct tgc gaa gaa tgt att aaa att ttg gat atg ggt ggg ggg
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly
 100 105 110
 ggt aaa att gat ttg ttg tgt ttt gaa gct ttt att acc aat gca aaa
 Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys
 115 120 125
 aaa tca ata aaa aaa tta aat ata aaa caa gga aaa tac aac aac aaa
 Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys
 130 135 140
 gaa ttt aca atg caa ata ctt aaa act aaa aat cca ttt tgg aca atg
 Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met
 145 150 155 160
 tgg gct aaa ata atc aaa aaa gat att tat tta aaa gcc ttc aac atg
 Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met
 165 170 175
 tta aat ctc aaa aaa gaa atc aaa ata aat atg gca gaa gat gcc tta
 Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu
 180 185 190
 tta tat tat cct ttg aca ata tta tct aat gaa ata ttt tac tta aca
 Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr
 195 200 205
 caa cct ttg tat acc cag cat gta aat agc aat tct ata aca aat aat
 Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn
 210 215 220
 att aat tct tta gaa gct aat att caa gaa cat aaa att gtt tta aat
 Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn
 225 230 235 240

gtt tta aaa tca att aaa aat aaa aaa aca cct cta tat ttt cta att		768	
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile			
245	250	255	
ata tat tta tta aaa att caa tta ttg aaa tat gaa caa aat ttt aat		816	
Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn			
260	265	270	
aaa aga aat ata aat ctt att tat tat aaa ata aat att tta tat caa		864	
Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln			
275	280	285	
aaa tat caa ttc aaa tgg aaa aaa ttt tta tat aat tta att ccg taa		912	
Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro			
290	295	300	
<210> 29			
<211> 303			
<212> PRT			
<213> Campylobacter jejuni			
<220>			
<223> Campylobacter glycosyltransferase B (CgtB) beta-1,3 galactosyltransferase from C. jejuni serotype O:2 (strain NCTC 11168)			
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1	5	10	15
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile			
20	25	30	
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile			
35	40	45	
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn			
50	55	60	
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val			
65	70	75	80
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu			
85	90	95	
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly			
100	105	110	
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys			
115	120	125	
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys			
130	135	140	
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met			
145	150	155	160
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met			
165	170	175	
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu			
180	185	190	
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr			
195	200	205	
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn			
210	215	220	
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn			
225	230	235	240
Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile			
245	250	255	

Ile	Tyr	Leu	Leu	Lys	Ile	Gln	Leu	Leu	Lys	Tyr	Glu	Gln	Asn	Phe	Asn
					260				265					270	
Lys	Arg	Asn	Ile	Asn	Leu	Ile	Tyr	Tyr	Lys	Ile	Asn	Ile	Leu	Tyr	Gln
					275			280					285		
Lys	Tyr	Gln	Phe	Lys	Trp	Lys	Lys	Phe	Leu	Tyr	Asn	Leu	Ile	Pro	
					290			295				300			

<210> 30
<211> 891
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(891)
<223> beta-1,3 galactosyl transferase from C. jejuni O:10

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Met				Lys	Ile	Ser	Ile	Ile	Leu	Pro	Thr	Tyr	Asn	Val	Glu	Gln	Tyr
1					5				10					15			
ata	gca	agg	gca	ata	gaa	agt	tgt	atc	aat	cag	act	ttt	aaa	aat	ata	96	
Ile	Ala	Arg	Ala	Ile	Glu	Ser	Cys	Ile	Asn	Gln	Thr	Phe	Lys	Asn	Ile		
				20				25					30				
gaa	ata	att	gta	gtt	gat	gat	tgt	gga	agt	gac	aaa	agt	ata	gat	ata	144	
Glu	Ile	Ile	Val	Val	Asp	Asp	Cys	Gly	Ser	Asp	Lys	Ser	Ile	Asp	Ile		
				35				40				45					
gtt	aaa	gaa	tat	gcc	aaa	aaa	gat	gat	aga	ata	aaa	atc	ata	cat	aat	192	
Val	Lys	Glu	Tyr	Ala	Lys	Asp	Asp	Arg	Ile	Lys	Ile	Ile	His	Asn			
	50				55				60								
gaa	gaa	aat	tta	aaa	ctt	tta	aga	gct	aga	tat	gaa	ggg	gta	aaa	gta	240	
Glu	Glu	Asn	Leu	Lys	Leu	Leu	Arg	Ala	Arg	Tyr	Glu	Gly	Val	Lys	Val		
	65				70				75				80				
gca	aac	tct	cct	tat	ata	atg	ttt	tta	gat	cct	gat	gat	tat	tta	gaa	288	
Ala	Asn	Ser	Pro	Tyr	Ile	Met	Phe	Leu	Asp	Pro	Asp	Asp	Tyr	Leu	Glu		
	85					90				95							
ctt	aat	gct	tgt	gaa	gaa	tgt	atg	aaa	att	tta	aaa	aac	aat	gaa	ata	336	
Leu	Asn	Ala	Cys	Glu	Glu	Cys	Met	Lys	Ile	Leu	Lys	Asn	Asn	Glu	Ile		
	100				105				105			110					
gat	tta	tta	ttt	ttt	aat	gca	ttt	gta	ttg	gaa	aat	aac	aat	aaa	ata	384	
Asp	Leu	Leu	Phe	Phe	Asn	Ala	Phe	Val	Leu	Glu	Asn	Asn	Asn	Lys	Ile		
	115				120				120			125					
gaa	aga	aag	ttg	aat	ttt	caa	gaa	aaa	tgt	tat	gta	aaa	aaa	gat	ttt	432	
Glu	Arg	Lys	Leu	Asn	Phe	Gln	Glu	Lys	Cys	Tyr	Val	Lys	Lys	Asp	Phe		
	130				135				135			140					
tta	aaa	gaa	cta	tta	aaa	act	aaa	aat	tta	ttt	tgg	aca	gtg	tgg	gca	480	
Leu	Lys	Glu	Leu	Leu	Lys	Thr	Lys	Asn	Leu	Phe	Trp	Thr	Val	Trp	Ala		
	145				150				150			155		160			

aaa gtc ata aaa aaa gaa tta tat ctc aag gct gtt ggt tta ata tcg	528
Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser	
165	170
	175
ctc gaa aat gct aaa ata aat atg gct gaa gat gtt tta tta tat tac	576
Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr	
180	185
	190
cct ttg ata aat att tca aat act ata ttt cac ttg agt aaa aat tta	624
Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu	
195	200
	205
tac aat tat caa ata aat aat ttc tct ata acc aaa aca tta aca ttg	672
Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu	
210	215
	220
caa aat ata aaa aca aat ata caa gaa caa gat aat gtt cta tat ctt	720
Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu	
225	230
	235
	240
cta aag aag atg caa tat aat tac aat ttt aac tta act ttg ctt aaa	768
Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys	
245	250
	255
tta att gag tat ttt tta tta att gaa aaa tac tca tta tca agc aag	816
Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys	
260	265
	270
cga aat gtt ctt tgt ttt aaa atc aat att ttt ttt aaa aaa atc caa	864
Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln	
275	280
	285
ttt aaa ttt tat cgc ttg ctg aag atg	891
Phe Lys Phe Tyr Arg Leu Leu Lys Met	
290	295
<210> 31	
<211> 297	
<212> PRT	
<213> Campylobacter jejuni	
<220>	
<223> beta-1,3 galactosyl transferase from C. jejuni O:10	
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1	5
	10
	15
Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile	
20	25
	30
Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile	
35	40
	45
Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn	
50	55
	60
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val	
65	70
	75
	80
Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu	
85	90
	95
Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile	
100	105
	110

Asp	Leu	Leu	Phe	Phe	Asn	Ala	Phe	Val	Leu	Glu	Asn	Asn	Lys	Ile	
	115						120				125				
Glu	Arg	Lys	Leu	Asn	Phe	Gln	Glu	Lys	Cys	Tyr	Val	Lys	Lys	Asp	Phe
	130					135				140					
Leu	Lys	Glu	Leu	Leu	Lys	Thr	Lys	Asn	Leu	Phe	Trp	Thr	Val	Trp	Ala
	145				150					155			160		
Lys	Val	Ile	Lys	Lys	Glu	Leu	Tyr	Leu	Lys	Ala	Val	Gly	Leu	Ile	Ser
				165				170				175			
Leu	Glu	Asn	Ala	Lys	Ile	Asn	Met	Ala	Glu	Asp	Val	Leu	Leu	Tyr	Tyr
		180					185				190				
Pro	Leu	Ile	Asn	Ile	Ser	Asn	Thr	Ile	Phe	His	Leu	Ser	Lys	Asn	Leu
	195					200					205				
Tyr	Asn	Tyr	Gln	Ile	Asn	Asn	Phe	Ser	Ile	Thr	Lys	Thr	Leu	Thr	Leu
	210					215				220					
Gln	Asn	Ile	Lys	Thr	Asn	Ile	Gln	Glu	Gln	Asp	Asn	Val	Leu	Tyr	Leu
	225				230				235			240			
Leu	Lys	Lys	Met	Gln	Tyr	Asn	Tyr	Asn	Phe	Asn	Leu	Thr	Leu	Leu	Lys
			245					250			255				
Leu	Ile	Glu	Tyr	Phe	Leu	Leu	Ile	Glu	Lys	Tyr	Ser	Leu	Ser	Ser	Lys
		260				265				270					
Arg	Asn	Val	Leu	Cys	Phe	Lys	Ile	Asn	Ile	Phe	Phe	Lys	Lys	Ile	Gln
	275					280					285				
Phe	Lys	Phe	Tyr	Arg	Leu	Leu	Lys	Met							
	290				295										

<210> 32

<211> 295

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> lipid A biosynthesis acyltransferase from *C. jejuni* OH4384

<400> 32

Met	Lys	Asn	Ser	Asp	Arg	Ile	Tyr	Leu	Ser	Leu	Tyr	Tyr	Ile	Leu	Lys
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Phe	Phe	Val	Thr	Phe	Met	Pro	Asp	Cys	Ile	Leu	His	Phe	Leu	Ala	Leu
					20			25				30			
Ile	Val	Ala	Arg	Ile	Ala	Phe	His	Leu	Asn	Lys	Lys	His	Arg	Lys	Ile
	35					40				45					
Ile	Asn	Thr	Asn	Leu	Gln	Ile	Cys	Phe	Pro	Gln	Tyr	Thr	Gln	Lys	Glu
	50					55				60					
Arg	Asp	Lys	Leu	Ser	Leu	Lys	Ile	Tyr	Glu	Asn	Phe	Ala	Gln	Phe	Gly
	65					70			75			80			
Ile	Asp	Cys	Leu	Gln	Asn	Gln	Asn	Thr	Thr	Lys	Glu	Lys	Ile	Leu	Asn
			85				90			95					
Lys	Val	Asn	Phe	Ile	Asn	Glu	Asn	Phe	Leu	Ile	Asp	Ala	Leu	Ala	Leu
			100				105				110				
Lys	Arg	Pro	Ile	Ile	Phe	Thr	Thr	Ala	His	Tyr	Gly	Asn	Trp	Glu	Ile
	115					120				125					
Leu	Ser	Leu	Ala	Tyr	Ala	Ala	Lys	Tyr	Gly	Ala	Ile	Ser	Ile	Val	Gly
	130					135				140					
Lys	Lys	Leu	Lys	Ser	Glu	Val	Met	Tyr	Glu	Ile	Leu	Ser	Gln	Ser	Arg
	145				150				155			160			
Thr	Gln	Phe	Asp	Ile	Glu	Leu	Ile	Asp	Lys	Lys	Gly	Gly	Ile	Arg	Gln
			165				170				175				
Met	Leu	Ser	Ala	Leu	Lys	Lys	Glu	Arg	Ala	Leu	Gly	Ile	Leu	Thr	Asp
	180					185				190					

Gln	Asp	Cys	Val	Glu	Asn	Glu	Ser	Val	Arg	Leu	Lys	Phe	Phe	Asn	Lys
195						200					205				
Glu	Val	Asn	Tyr	Gln	Met	Gly	Ala	Ser	Leu	Ile	Ala	Gln	Arg	Ser	Asn
210						215					220				
Ala	Leu	Ile	Ile	Pro	Val	Tyr	Ala	Tyr	Lys	Glu	Gly	Gly	Lys	Phe	Cys
225						230				235				240	
Ile	Glu	Phe	Phe	Lys	Ala	Lys	Asp	Ser	Gln	Asn	Ala	Ser	Leu	Glu	Glu
	245					250				250			255		
Leu	Thr	Leu	Tyr	Gln	Ala	Gln	Ser	Cys	Glu	Glu	Met	Ile	Lys	Lys	Arg
	260					265				265			270		
Pro	Trp	Glu	Tyr	Phe	Phe	His	Arg	Arg	Phe	Ala	Ser	Tyr	Asn	Glu	
	275					280						285			
Glu	Ile	Tyr	Lys	Gly	Ala	Lys									
	290					295									

<210> 33

<211> 418

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> glycosyltransferase from *C. jejuni* OH4384 (ORF 3a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 33

Met	Asn	Leu	Lys	Gln	Ile	Ser	Val	Ile	Ile	Val	Lys	Asn	Ala	Glu	
1						5				10				15	
Gln	Thr	Leu	Leu	Glu	Cys	Leu	Asn	Ser	Leu	Lys	Asp	Phe	Asp	Glu	Ile
						20				25				30	
Ile	Leu	Leu	Asn	Asn	Glu	Ser	Ser	Asp	Asn	Thr	Leu	Lys	Ile	Ala	Asn
						35				40				45	
Glu	Phe	Lys	Lys	Asp	Phe	Ala	Asn	Leu	Tyr	Ile	Tyr	His	Asn	Ala	Phe
						50				55				60	
Ile	Gly	Phe	Gly	Ala	Leu	Lys	Asn	Leu	Ala	Leu	Ser	Tyr	Ala	Lys	Asn
						65				70				75	
Asp	Trp	Ile	Leu	Ser	Ile	Asp	Ala	Asp	Glu	Val	Leu	Glu	Asn	Glu	Cys
						85				90				95	
Ile	Lys	Glu	Leu	Lys	Asn	Leu	Lys	Leu	Gln	Glu	Asp	Asn	Ile	Ile	Ala
						100				105				110	
Leu	Ser	Arg	Lys	Asn	Leu	Tyr	Lys	Gly	Glu	Trp	Ile	Lys	Ala	Cys	Gly
						115				120				125	
Trp	Trp	Pro	Asp	Tyr	Val	Leu	Arg	Ile	Phe	Asn	Lys	Asn	Phe	Thr	Arg
						130				135				140	
Phe	Asn	Asp	Asn	Leu	Val	His	Glu	Ser	Leu	Val	Leu	Pro	Ser	Asn	Ala
						145				150				155	
Lys	Lys	Ile	Tyr	Leu	Lys	Asn	Gly	Leu	Lys	His	Tyr	Ser	Tyr	Lys	Asp
						165				170				175	
Ile	Ser	His	Leu	Ile	Asp	Lys	Met	Gln	Tyr	Tyr	Ser	Ser	Leu	Trp	Ala
						180				185				190	
Lys	Gln	Asn	Ile	His	Lys	Lys	Ser	Gly	Val	Leu	Lys	Ala	Asn	Leu	Arg
						195				200				205	
Ala	Phe	Trp	Thr	Phe	Phe	Arg	Asn	Tyr	Phe	Leu	Lys	Asn	Gly	Phe	Leu
						210				215				220	
Tyr	Gly	Tyr	Lys	Gly	Phe	Ile	Ile	Ser	Val	Cys	Ser	Ala	Leu	Gly	Thr
						225				230				235	
Phe	Phe	Lys	Tyr	Met	Lys	Leu	Tyr	Glu	Leu	Gln	Arg	Gln	Lys	Pro	Lys
						245				250				255	
Thr	Cys	Ala	Leu	Ile	Ile	Ile	Thr	Tyr	Asn	Gln	Lys	Glu	Arg	Leu	Lys
						260				265				270	

Leu Val Leu Asp Ser Val Lys Asn Leu Ala Phe Leu Pro Asn Glu Val
 275 280 285
 Leu Ile Ala Asp Asp Gly Ser Lys Glu Asp Thr Ala Arg Leu Ile Glu
 290 295 300
 Glu Tyr Gln Lys Asp Phe Pro Cys Pro Leu Lys His Ile Trp Gln Glu
 305 310 315 320
 Asp Glu Gly Phe Lys Leu Ser Lys Ser Arg Asn Lys Thr Ile Lys Asn
 325 330 335
 Ala Asp Ser Glu Tyr Ile Ile Val Ile Asp Gly Asp Met Ile Leu Glu
 340 345 350
 Lys Asp Phe Ile Lys Glu His Leu Glu Phe Ala Gln Arg Lys Leu Phe
 355 360 365
 Leu Gln Gly Ser Arg Val Ile Leu Asn Lys Lys Glu Ser Glu Glu Ile
 370 375 380
 Leu Asn Lys Asp Asp Tyr Arg Ile Ile Phe Asn Lys Lys Asp Phe Lys
 385 390 395 400
 Ser Ser Lys Asn Ser Phe Leu Ala Lys Ile Phe Tyr Ser Leu Ser Lys
 405 410 415
 Lys Arg

<210> 34

<211> 389

<212> PRT

<213> Campylobacter jejuni

<220>

<223> glycosyltransferase of C. jejuni OH4384 (ORF 4a of
lipooligosaccharide (LOS) biosynthesis locus)

<400> 34

Met Lys Lys Ile Gly Val Val Ile Pro Ile Tyr Asn Val Glu Lys Tyr
 1 5 10 15
 Leu Arg Glu Cys Leu Asp Ser Val Ile Asn Gln Thr Tyr Thr Asn Leu
 20 25 30
 Glu Ile Ile Leu Val Asn Asp Gly Ser Thr Asp Glu His Ser Leu Asn
 35 40 45
 Ile Ala Lys Glu Tyr Thr Leu Lys Asp Lys Arg Ile Thr Leu Phe Asp
 50 55 60
 Lys Lys Asn Gly Gly Leu Ser Ser Ala Arg Asn Ile Gly Ile Glu Tyr
 65 70 75 80
 Phe Ser Gly Glu Tyr Lys Leu Lys Asn Lys Thr Gln His Ile Lys Glu
 85 90 95
 Asn Ser Leu Ile Glu Phe Gln Leu Asp Gly Asn Asn Pro Tyr Asn Ile
 100 105 110
 Tyr Lys Ala Tyr Lys Ser Ser Gln Ala Phe Asn Asn Glu Lys Asp Leu
 115 120 125
 Thr Asn Phe Thr Tyr Pro Ser Ile Asp Tyr Ile Ile Phe Leu Asp Ser
 130 135 140
 Asp Asn Tyr Trp Lys Leu Asn Cys Ile Glu Glu Cys Val Ile Arg Met
 145 150 155 160
 Lys Asn Val Asp Val Leu Trp Phe Asp His Asp Cys Thr Tyr Glu Asp
 165 170 175
 Asn Ile Lys Asn Lys His Lys Lys Thr Arg Met Glu Ile Phe Asp Phe
 180 185 190
 Lys Lys Glu Cys Ile Ile Thr Pro Lys Glu Tyr Ala Asn Arg Ala Leu
 195 200 205
 Ser Val Gly Ser Arg Asp Ile Ser Phe Gly Trp Asn Gly Met Ile Asp
 210 215 220
 Phe Asn Phe Leu Lys Gln Ile Lys Leu Lys Phe Ile Asn Phe Ile Ile
 225 230 235 240

Asn	Glu	Asp	Ile	His	Phe	Gly	Ile	Leu	Phe	Ala	Ser	Ala	Asn	Lys		
					245				250					255		
Ile	Tyr	Val	Leu	Ser	Gln	Lys	Leu	Tyr	Leu	Cys	Arg	Leu	Arg	Ala	Asn	
					260				265					270		
Ser	Ile	Ser	Asn	His	Asp	Lys	Lys	Ile	Thr	Lys	Ala	Asn	Val	Ser	Glu	
					275				280					285		
Tyr	Phe	Lys	Asp	Ile	Tyr	Glu	Thr	Phe	Gly	Glu	Asn	Ala	Lys	Glu	Ala	
					290				295					300		
Lys	Asn	Tyr	Leu	Lys	Ala	Ala	Ser	Arg	Val	Ile	Thr	Ala	Leu	Lys	Leu	
					305				310					315		320
Ile	Glu	Phe	Phe	Lys	Asp	Gln	Lys	Asn	Glu	Asn	Ala	Leu	Ala	Ile	Lys	
					325				330					335		
Glu	Thr	Phe	Leu	Pro	Cys	Tyr	Ala	Lys	Lys	Ala	Leu	Met	Ile	Lys	Lys	
					340				345					350		
Phe	Lys	Lys	Asp	Pro	Leu	Asn	Leu	Lys	Glu	Gln	Leu	Val	Leu	Ile	Lys	
					355				360					365		
Pro	Phe	Ile	Gln	Thr	Lys	Leu	Pro	Tyr	Asp	Ile	Trp	Lys	Phe	Trp	Gln	
					370				375					380		
Lys	Ile	Lys	Asn	Ile												
					385											

<210> 35

<211> 346

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> sialic acid synthase from *C. jejuni* OH4384 (ORF 8a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 35

Met	Lys	Glu	Ile	Lys	Ile	Gln	Asn	Ile	Ile	Ser	Glu	Glu	Lys	Ala	
1					5				10					15	
Pro	Leu	Val	Val	Pro	Glu	Ile	Gly	Ile	Asn	His	Asn	Gly	Ser	Leu	Glu
					20				25					30	
Leu	Ala	Lys	Ile	Met	Val	Asp	Ala	Ala	Phe	Ser	Thr	Gly	Ala	Lys	Ile
					35				40					45	
Ile	Lys	His	Gln	Thr	His	Ile	Val	Glu	Asp	Glu	Met	Ser	Lys	Ala	Ala
					50				55					60	
Lys	Lys	Val	Ile	Pro	Gly	Asn	Ala	Lys	Ile	Ser	Ile	Tyr	Glu	Ile	Met
					65				70					80	
Gln	Lys	Cys	Ala	Leu	Asp	Tyr	Lys	Asp	Glu	Leu	Ala	Leu	Lys	Glu	Tyr
					85				90					95	
Thr	Glu	Lys	Leu	Gly	Leu	Val	Tyr	Leu	Ser	Thr	Pro	Phe	Ser	Arg	Ala
					100				105					110	
Gly	Ala	Asn	Arg	Leu	Glu	Asp	Met	Gly	Val	Ser	Ala	Phe	Lys	Ile	Gly
					115				120					125	
Ser	Gly	Glu	Cys	Asn	Asn	Tyr	Pro	Leu	Ile	Lys	His	Ile	Ala	Ala	Phe
					130				135					140	
Lys	Lys	Pro	Met	Ile	Val	Ser	Thr	Gly	Met	Asn	Ser	Ile	Glu	Ser	Ile
					145				150					160	
Lys	Pro	Thr	Val	Lys	Ile	Leu	Leu	Asp	Asn	Glu	Ile	Pro	Phe	Val	Leu
					165				170					175	
Met	His	Thr	Thr	Asn	Leu	Tyr	Pro	Thr	Pro	His	Asn	Leu	Val	Arg	Leu
					180				185					190	
Asn	Ala	Met	Leu	Glu	Leu	Lys	Lys	Glu	Phe	Ser	Cys	Met	Val	Gly	Leu
					195				200					205	
Ser	Asp	His	Thr	Thr	Asp	Asn	Leu	Ala	Cys	Leu	Gly	Ala	Val	Ala	Leu
					210				215					220	

Gly	Ala	Cys	Val	Leu	Glu	Arg	His	Phe	Thr	Asp	Ser	Met	His	Arg	Ser
225				230					235					240	
Gly	Pro	Asp	Ile	Val	Cys	Ser	Met	Asp	Thr	Gln	Ala	Leu	Lys	Glu	Leu
					245				250					255	
Ile	Ile	Gln	Ser	Glu	Gln	Met	Ala	Ile	Met	Arg	Gly	Asn	Asn	Glu	Ser
					260			265			270				
Lys	Lys	Ala	Ala	Lys	Gln	Glu	Gln	Val	Thr	Ile	Asp	Phe	Ala	Phe	Ala
					275			280			285				
Ser	Val	Val	Ser	Ile	Lys	Asp	Ile	Lys	Lys	Gly	Glu	Val	Leu	Ser	Met
					290			295			300				
Asp	Asn	Ile	Trp	Val	Lys	Arg	Pro	Gly	Leu	Gly	Gly	Ile	Ser	Ala	Ala
					305			310			315			320	
Glu	Phe	Glu	Asn	Ile	Leu	Gly	Lys	Lys	Ala	Leu	Arg	Asp	Ile	Glu	Asn
					325			330						335	
Asp	Thr	Gln	Leu	Ser	Tyr	Glu	Asp	Phe	Ala						
					340			345							

<210> 36
<211> 352
<212> PRT
<213> Campylobacter jejuni

<220>
<223> enzyme involved in sialic acid biosynthesis from
C. jejuni OH4384 (ORF 9a of lipooligosaccharide (LOS)
biosynthesis locus)

<400>	36														
Met	Tyr	Arg	Val	Gln	Asn	Ser	Ser	Glu	Phe	Glu	Leu	Tyr	Ile	Phe	Ala
1				5				10						15	
Thr	Gly	Met	His	Leu	Ser	Lys	Asn	Phe	Gly	Tyr	Thr	Val	Lys	Glu	Leu
								20			25			30	
Tyr	Lys	Asn	Gly	Phe	Lys	Asn	Ile	Tyr	Glu	Phe	Ile	Asn	Tyr	Asp	Lys
							35			40			45		
Tyr	Phe	Ser	Thr	Asp	Lys	Ala	Leu	Ala	Thr	Thr	Ile	Asp	Gly	Phe	Ser
							50			55			60		
Arg	Tyr	Val	Asn	Glu	Leu	Lys	Pro	Asp	Leu	Ile	Val	Val	His	Gly	Asp
							65			70			75		80
Arg	Ile	Glu	Pro	Leu	Ala	Ala	Ile	Val	Gly	Ala	Leu	Asn	Asn	Ile	
							85			90			95		
Leu	Val	Ala	His	Ile	Glu	Gly	Glu	Ile	Ser	Gly	Thr	Ile	Asp	Asp	
							100			105			110		
Ser	Leu	Arg	His	Ala	Ile	Ser	Lys	Leu	Ala	His	Ile	His	Leu	Val	Asn
							115			120			125		
Asp	Glu	Phe	Ala	Lys	Arg	Arg	Leu	Met	Gln	Leu	Gly	Glu	Asp	Glu	Lys
							130			135			140		
Ser	Ile	Phe	Ile	Ile	Gly	Ser	Pro	Asp	Leu	Glu	Leu	Leu	Asn	Asp	Asn
							145			150			155		160
Lys	Ile	Ser	Leu	Asn	Glu	Ala	Lys	Lys	Tyr	Tyr	Asp	Ile	Asn	Tyr	Glu
							165			170			175		
Asn	Tyr	Ala	Leu	Leu	Met	Phe	His	Pro	Val	Thr	Thr	Glu	Ile	Thr	Ser
							180			185			190		
Ile	Lys	Asn	Gln	Ala	Asp	Asn	Leu	Val	Lys	Ala	Leu	Ile	Gln	Ser	Asn
							195			200			205		
Lys	Asn	Tyr	Ile	Val	Ile	Tyr	Pro	Asn	Asn	Asp	Leu	Gly	Phe	Glu	Leu
							210			215			220		
Ile	Leu	Gln	Ser	Tyr	Glu	Glu	Leu	Lys	Asn	Asn	Pro	Arg	Phe	Lys	Leu
							225			230			235		240
Phe	Pro	Ser	Leu	Arg	Phe	Glu	Tyr	Phe	Ile	Thr	Leu	Leu	Lys	Asn	Ala
							245			250			255		

Asp	Phe	Ile	Ile	Gly	Asn	Ser	Ser	Cys	Ile	Leu	Lys	Glu	Ala	Leu	Tyr
	260				265						270				
Leu	Lys	Thr	Ala	Gly	Ile	Leu	Val	Gly	Ser	Arg	Gln	Asn	Gly	Arg	Leu
	275					280				285					
Gly	Asn	Glu	Asn	Thr	Leu	Lys	Val	Asn	Ala	Asn	Ser	Asp	Glu	Ile	Leu
	290					295				300					
Lys	Ala	Ile	Asn	Thr	Ile	His	Lys	Lys	Gln	Asp	Leu	Phe	Ser	Ala	Lys
	305					310			315			320			
Leu	Glu	Ile	Leu	Asp	Ser	Ser	Lys	Leu	Phe	Phe	Glu	Tyr	Leu	Gln	Ser
					325			330			335				
Gly	Glu	Phe	Phe	Lys	Leu	Asn	Thr	Gln	Lys	Val	Phe	Lys	Asp	Ile	Lys
					340			345			350				

<210> 37
<211> 221
<212> PRT
<213> Campylobacter jejuni

<220>
<223> CMP-sialic acid synthetase from C. jejuni OH4384
(ORF 10a of lipooligosaccharide (LOS) biosynthesis
locus)

<400>	37														
Met	Ser	Leu	Ala	Ile	Ile	Pro	Ala	Arg	Gly	Gly	Ser	Lys	Gly	Ile	Lys
1				5					10						15
Asn	Lys	Asn	Leu	Val	Leu	Leu	Asn	Asn	Lys	Pro	Leu	Ile	Tyr	Tyr	Thr
					20			25					30		
Ile	Lys	Ala	Ala	Leu	Asn	Thr	Lys	Ser	Ile	Ser	Lys	Val	Val	Val	Ser
					35			40					45		
Ser	Asp	Ser	Asp	Glu	Ile	Leu	Asn	Tyr	Ala	Lys	Ser	Gln	Asn	Val	Asp
					50			55				60			
Ile	Leu	Lys	Arg	Pro	Ile	Ser	Leu	Ala	Gln	Asp	Asn	Thr	Thr	Ser	Asp
					65			70			75				80
Lys	Val	Leu	Leu	His	Ala	Leu	Lys	Phe	Tyr	Lys	Asp	Tyr	Glu	Asp	Val
						85			90						95
Val	Phe	Leu	Gln	Pro	Thr	Ser	Pro	Leu	Arg	Thr	Asn	Ile	His	Ile	Asp
					100			105							110
Glu	Ala	Phe	Asn	Leu	Tyr	Lys	Asn	Ser	Asn	Ala	Asn	Ala	Leu	Ile	Ser
					115			120					125		
Val	Ser	Glu	Cys	Asp	Asn	Lys	Ile	Leu	Lys	Ala	Phe	Val	Cys	Asn	Glu
					130			135					140		
Tyr	Gly	Asp	Leu	Ala	Gly	Ile	Cys	Asn	Asp	Glu	Tyr	Pro	Phe	Met	Pro
						145		150			155				160
Arg	Gln	Lys	Leu	Pro	Lys	Thr	Tyr	Met	Ser	Asn	Gly	Ala	Ile	Tyr	Ile
						165			170				175		
Leu	Lys	Ile	Lys	Glu	Phe	Leu	Asn	Asn	Pro	Ser	Phe	Leu	Gln	Ser	Lys
						180		185					190		
Thr	Lys	His	Phe	Leu	Met	Asp	Glu	Ser	Ser	Ser	Leu	Asp	Ile	Asp	Cys
					195			200					205		
Leu	Glu	Asp	Leu	Lys	Lys	Ala	Glu	Gln	Ile	Trp	Lys	Lys			
					210			215			220				

<210> 38
<211> 277
<212> PRT
<213> Campylobacter jejuni

<220>
<223> acetyltransferase from C. jejuni OH4384 (ORF 11a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 38

Met	Glu	Lys	Ile	Thr	Leu	Lys	Cys	Asn	Lys	Asn	Ile	Leu	Asn	Leu	Leu
1						5			10						15
Lys	Gln	Tyr	Asn	Ile	Tyr	Thr	Lys	Thr	Tyr	Ile	Glu	Asn	Pro	Arg	Arg
						20			25						30
Phe	Ser	Arg	Leu	Lys	Thr	Lys	Asp	Phe	Ile	Thr	Phe	Pro	Leu	Glu	Asn
						35			40						45
Asn	Gln	Leu	Glu	Ser	Val	Ala	Gly	Leu	Gly	Ile	Glu	Glu	Tyr	Cys	Ala
						50			55						60
Phe	Lys	Phe	Ser	Asn	Ile	Leu	His	Glu	Met	Asp	Ser	Phe	Ser	Phe	Ser
						65			70			75			80
Gly	Ser	Phe	Leu	Pro	His	Tyr	Thr	Lys	Val	Gly	Arg	Tyr	Cys	Ser	Ile
						85			90						95
Ser	Asp	Gly	Val	Ser	Met	Phe	Asn	Phe	Gln	His	Pro	Met	Asp	Arg	Ile
						100			105						110
Ser	Thr	Ala	Ser	Phe	Thr	Tyr	Glu	Thr	Asn	His	Ser	Phe	Ile	Asn	Asp
						115			120						125
Ala	Cys	Gln	Asn	His	Ile	Asn	Lys	Thr	Phe	Pro	Ile	Val	Asn	His	Asn
						130			135						140
Pro	Ser	Ser	Ser	Ile	Thr	His	Leu	Ile	Ile	Gln	Asp	Asp	Val	Trp	Ile
						145			150			155			160
Gly	Lys	Asp	Val	Leu	Leu	Lys	Gln	Gly	Ile	Thr	Leu	Gly	Thr	Gly	Cys
						165			170						175
Val	Ile	Gly	Gln	Arg	Ala	Val	Val	Thr	Lys	Asp	Val	Pro	Pro	Tyr	Ala
						180			185						190
Ile	Val	Ala	Gly	Ile	Pro	Ala	Lys	Ile	Ile	Lys	Tyr	Arg	Phe	Asp	Glu
						195			200			205			
Lys	Thr	Ile	Glu	Arg	Leu	Leu	Lys	Ile	Gln	Trp	Trp	Lys	Tyr	His	Phe
						210			215			220			
Ala	Asp	Phe	Tyr	Asp	Ile	Asp	Leu	Asn	Leu	Lys	Ile	Asn	Gln	Tyr	Leu
						225			230			235			240
Asp	Leu	Leu	Glu	Glu	Lys	Ile	Ile	Lys	Lys	Ser	Ile	Ser	Tyr	Tyr	Asn
						245			250						255
Pro	Asn	Lys	Leu	Tyr	Phe	Arg	Asp	Ile	Leu	Glu	Leu	Lys	Ser	Lys	Lys
						260			265						270
Ile	Phe	Asn	Leu	Phe											
						275									

<210> 39
<211> 270
<212> PRT
<213> Campylobacter jejuni

<220>
<223> glycosyltransferase from C. jejuni OH4384 (ORF 12a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 39

Met	Pro	Gln	Leu	Ser	Ile	Ile	Pro	Leu	Phe	Asn	Ser	Cys	Asp	Phe	
1						5			10					15	
Ile	Ser	Arg	Ala	Leu	Gln	Ser	Cys	Ile	Asn	Gln	Thr	Leu	Lys	Asp	Ile
						20			25					30	
Glu	Ile	Leu	Ile	Ile	Asp	Asp	Lys	Ser	Lys	Asp	Asn	Ser	Leu	Asn	Met
						35			40			45			
Val	Leu	Glu	Phe	Ala	Lys	Lys	Asp	Pro	Arg	Ile	Lys	Ile	Phe	Gln	Asn
						50			55			60			

Glu	Glu	Asn	Leu	Gly	Thr	Phe	Ala	Ser	Arg	Asn	Leu	Gly	Val	Leu	His
65				70					75					80	
Ser	Ser	Ser	Asp	Phe	Ile	Met	Phe	Leu	Asp	Ser	Asp	Asp	Phe	Leu	Thr
				85				90						95	
Pro	Asp	Ala	Cys	Glu	Ile	Ala	Phe	Lys	Glu	Met	Lys	Lys	Gly	Phe	Asp
			100				105							110	
Leu	Leu	Cys	Phe	Asp	Ala	Phe	Val	His	Arg	Val	Lys	Thr	Lys	Gln	Phe
			115				120							125	
Tyr	Arg	Phe	Lys	Gln	Asp	Glu	Val	Phe	Asn	Gln	Lys	Glu	Phe	Leu	Glu
	130			135			140								
Phe	Leu	Ser	Lys	Gln	Arg	His	Phe	Cys	Trp	Ser	Val	Trp	Ala	Lys	Cys
145				150					155					160	
Phe	Lys	Lys	Asp	Ile	Ile	Leu	Lys	Ser	Phe	Glu	Lys	Ile	Lys	Ile	Asp
			165				170							175	
Glu	Arg	Leu	Asn	Tyr	Gly	Glu	Asp	Val	Leu	Phe	Cys	Tyr	Ile	Tyr	Phe
			180				185							190	
Met	Phe	Cys	Glu	Lys	Ile	Ala	Val	Phe	Lys	Thr	Cys	Ile	Tyr	His	Tyr
			195				200							205	
Glu	Phe	Asn	Pro	Asn	Gly	Arg	Tyr	Glu	Asn	Lys	Asn	Lys	Glu	Ile	Leu
	210			215					220						
Asn	Gln	Asn	Tyr	His	Asp	Lys	Lys	Ser	Asn	Glu	Ile	Ile	Lys	Lys	
225				230				235						240	
Leu	Ser	Lys	Glu	Phe	Ala	His	Asp	Glu	Phe	His	Gln	Lys	Leu	Phe	Glu
			245				250							255	
Val	Leu	Lys	Arg	Glu	Glu	Ala	Gly	Val	Lys	Asn	Arg	Leu	Lys		
			260				265							270	

<210> 40

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ42 primer in
heptosyltransferase-II used to amplify LPS core
biosynthesis locus

<400> 40

gccattaccg tatcgctaa ccagg

25

<210> 41

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ43 primer in
heptosyltransferase-I used to amplify LPS core
biosynthesis locus

<400> 41

aaagaataacg aatttgctaa agagg

25

<210> 42

<211> 41

<212> DNA

<213> Artificial Sequence

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<220>
<223> Description of Artificial Sequence:CJ-106 3'
      primer used to amplify and clone ORF 5a

<400> 42
ccttaggtcga cttaaaaacaa tgttaagaat attttttta g           41

<210> 43
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ-157 5'
      primer used to amplify and clone ORF 5a

<400> 43
cttaggaggt catatgctat ttcaatcata ctttgtg           37

<210> 44
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ-105 3'
      primer used to amplify and clone ORF 6a

<400> 44
ccttaggtcga cctctaaaaa aaatattctt aacattg           37

<210> 45
<211> 39
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ-133 5'
      primer used to amplify and clone ORF 6a

<400> 45
cttaggaggt catatgtta aaatttcaat catcttacc           39

<210> 46
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ-131 5'
      primer used to amplify and clone ORF 7a

<400> 46
cttaggaggt catatgaaaa aagttattat tgctggaaat g           41

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<210> 47
<211> 41
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:CJ-132 3'
      primer used to amplify and clone ORF 7a

<400> 47
ccttaggtcgatttcc ttggaaataa tgctttatat c           41

<210> 48
<211> 322
<212> PRT
<213> Campylobacter jejuni

<220>
<223> Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
      from C. jejuni OH4384

<400> 48
Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met
    1          5          10          15
Gln Asn Ile Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
    20         25          30
Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
    35         40          45
Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
    50         55          60
Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
    65         70          75          80
Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe
    85         90          95
Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn
   100        105        110
Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys
   115        120        125
Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg
   130        135        140
Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr
   145        150        155        160
Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile
   165        170        175
Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly
   180        185        190
Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile
   195        200        205
Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala
   210        215        220
Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn
   225        230        235        240
Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn
   245        250        255
Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn
   260        265        270
Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu
   275        280        285
His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val
   290        295        300

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Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His
305 310 315 320
Leu Ser

<210> 49
<211> 231
<212> PRT
<213> Haemophilus influenzae

<220>
<223> putative ORF from GenBank #U32720

<400> 49
Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu
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Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn
20 25 30
Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn
35 40 45
Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
50 55 60
Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
65 70 75 80
Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
85 90 95
Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
100 105 110
Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
115 120 125
Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
130 135 140
Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
145 150 155 160
Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
165 170 175
Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
180 185 190
Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
195 200 205
Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
210 215 220
Leu Lys Ser Arg Lys Trp Asp
225 230